OIPE

RAW SEQUENCE LISTING   DATE: 01/11/2002
PATENT APPLICATION: US/10/020,095   TIME: 12:55:59

Input Set : **A:\LEX-0282-USA SEQLIST.txt**
Output Set: **N:\CRF3\01112002\J020095.raw**

ENTERED

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   3 <110> APPLICANT: Walke, D. Wade
   4        Scoville, John
   5        Turner, C. Alexander Jr.
   7 <120> TITLE OF INVENTION: Novel Human Alpha Macroglobulin Family Proteins and
Polynucleotides
   8        Encoding the Same
  10 <130> FILE REFERENCE: LEX-0282-USA
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/020,095
C--> 12 <141> CURRENT FILING DATE: 2001-12-14
  12 <150> PRIOR APPLICATION NUMBER: US 60/255,566
  13 <151> PRIOR FILING DATE: 2000-12-14
  15 <160> NUMBER OF SEQ ID NOS: 5
  17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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  20 <211> LENGTH: 4338
  21 <212> TYPE: DNA
  22 <213> ORGANISM: homo sapiens
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  28 gagctgctca agacagcatc aaacctcact gtctctgtcc tggaagcaga aggagtcttt     240
  29 gaaaaaggct ctttttaagac acttactctt ccatcactac ctctgaacag tgcagatgag     300
  30 atttatgagc tacgtgtaac cggacgtacc caggatgaga ttttattctc taatagtacc     360
  31 cgcttatcat ttgagaccaa gagaatatct gtcttcattc aaacagacaa ggccttatac     420
  32 aagccaaagc aagaagtgaa gtttcgcatt gttacactct ctcagatttt taagccttac     480
  33 aaaacctctt taaacattct cattaaggac cccaaatcaa atttgatcca acagtggttg     540
  34 tcacaacaaa gtgatcttgg agtcatttcc aaaacttttc agctatcttc ccatccaata     600
  35 cttggtgact ggtctattca agttcaagtg aatgaccaga catattatca atcatttcag     660
  36 gtttcagaat atgtattacc aaaatttgaa gtgactttgc agacaccatt atattgttct     720
  37 atgaattcta agcatttaaa tggtaccatc acggcaaagt atacatatgg gaagccagtg     780
  38 aaaggagacg taacgcttac attttttacct ttatcctttt ggggaaagaa gaaaaatatt     840
  39 acaaaaacat ttaagataaa tggatctgca aacttctctt ttaatgatga agagatgaaa     900
  40 aatgtaatgg attcttcaaa tggactttct gaatacctgg atctatcttc ccctggacca     960
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  42 aatgtgttct tcaagcaaca tgattacatc attgagtttt ttgattatac tactgtcttg    1080
  43 aagccatctc tcaacttcac agccactgtg aaggtaactc gtgctgatgg caaccaactg    1140
  44 actcttgaag aaagaagaaa taatgtagtc ataacagtga cacagagaaa ctatactgag    1200
  45 tactggagcg gatctaacag tggaaatcag aaaatggaag ctgttcagaa aataaattat    1260
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  47 ctacagttga aggcctattt ccttggtagt aaaagtagca tggcagttca tagtctgtttt    1380
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  53 ctatattgga gtaaagtgaa agctgaacca tctgagaaag tctctcttag gatctctgtg    1740
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56 tattatttag gcatgttcat gaattctttt gcagtctttc aggaatgtgg actctgggta   1920
57 ttgacagatg caaacctcac gaaggattat attgatggtg tttatgacaa tgcagaatat   1980
58 gctgagaggt ttatggagga aaatgaagga catattgtag atattcatga cttttctttg   2040
59 ggtagcagtc cacatgtccg aaagcatttt ccagagactt ggatttggct agacaccaac   2100
60 atgggttaca ggatttacca agaatttgaa gtaactgtac ctgattctat cacttcttgg   2160
61 gtggctactg gtttttgtgat ctctgaggac ctgggtcttg gactaacaac tactccagtg   2220
62 gagctccaag ccttccaacc atttttcatt tttttgaatc ttccctactc tgttatcaga   2280
63 ggtgaagaat ttgctttgga aataactata ttcaattatt tgaaagatgc cactgaggtt   2340
64 aaggtaatca ttgagaaaag tgacaaattt gatattctaa tgacttcaag tgaaataaat   2400
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72 aaaaagaaac aactgacaga taatttgaaa gaaaaagctc tttcatttat gaggcaaggt   2880
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82 gatattgaag ttgcagccta tgcactgctc tcacacttct tacaatttca gacttctgag   3480
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101 <212> TYPE: PRT
102 <213> ORGANISM: homo sapiens
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108          20                  25                  30
109  Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
110          35                  40                  45
111  Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
112      50                  55                  60
113  Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
114  65                  70                  75                  80
115  Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
116              85                  90                  95
117  Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
118              100                 105                 110
119  Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
120              115                 120                 125
121  Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
122          130                 135                 140
123  Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
124  145                 150                 155                 160
125  Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
126              165                 170                 175
127  Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr
128              180                 185                 190
129  Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val
130          195                 200                 205
131  Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr
132      210                 215                 220
133  Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser
134  225                 230                 235                 240
135  Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr
136              245                 250                 255
137  Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser
138          260                 265                 270
139  Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly
140          275                 280                 285
141  Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp
142      290                 295                 300
143  Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Ser Pro Gly Pro
144  305                 310                 315                 320
145  Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg
146          325                 330                 335
147  Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu
148          340                 345                 350
149  Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala
150          355                 360                 365
151  Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu
152      370                 375                 380
153  Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu
154  385                 390                 395                 400
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155 Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln
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157 Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe
158              420              425              430
159 Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu
160          435              440              445
161 Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser
162      450              455              460
163 Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
164 465              470              475              480
165 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
166          485              490              495
167 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
168          500              505              510
169 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
170          515              520              525
171 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
172      530              535              540
173 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
174 545              550              555              560
175 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
176              565              570              575
177 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
178              580              585              590
179 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
180          595              600              605
181 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
182      610              615              620
183 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
184 625              630              635              640
185 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
186              645              650              655
187 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
188          660              665              670
189 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
190          675              680              685
191 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Tyr Arg
192      690              695              700
193 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
194 705              710              715              720
195 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
196              725              730              735
197 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu
198              740              745              750
199 Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile
200          755              760              765
201 Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile
202      770              775              780
203 Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn
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208                   820                   825                   830
209 Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Val Thr Gln Met
210               835                   840                   845
211 Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile
212       850                   855                   860
213 Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu
214 865                   870                   875                   880
215 Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln
216                   885                   890                   895
217 Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala
218               900                   905                   910
219 Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn
220               915                   920                   925
221 Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln
222       930                   935                   940
223 Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly
224 945                   950                   955                   960
225 Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala
226               965                   970                   975
227 Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val
228               980                   985                   990
229 Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn
230       995                   1000                  1005
231 Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn
232       1010                  1015                  1020
233 Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
234 1025                  1030                  1035                  1040
235 Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
236               1045                  1050                  1055
237 Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
238               1060                  1065                  1070
239 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
240           1075                  1080                  1085
241 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
242       1090                  1095                  1100
243 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
244 1105                  1110                  1115                  1120
245 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
246               1125                  1130                  1135
247 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
248           1140                  1145                  1150
249 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
250           1155                  1160                  1165
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252       1170                  1175                  1180
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VERIFICATION SUMMARY   DATE: 01/11/2002
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date